

SEQUENCE LISTING

<110> Meyers, Rachel
MacBeth, Kyle
Tsai, Fong-Ying

<1200> 4737, A NOVEL HUMAN
GALACTOSYLTRANSFERASE AND USES THEREOF

<1,500 MN I-188

<1:0> 61/229, 529
<1:1> 110-03-31

<1 6> 1

<1> FastSEQ for Windows Version 4.0

2110

<2> 1 > 1252

<212> DNA

<213> Homo sapiens

2.3

$\leq 2.1 \times 10^3$

(2, 2, 4, 5, 6) . . . (15, 9, 2)

1400

REFERENCES

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Met Arg Met Leu Val Ser
1 5

1

20

ggc agt aga gtc aaa aaa tgg cag tta att att cag tta ttt gct act 524
 Gly Arg Arg Val Lys Lys Trp Gln Leu Ile Ile Gln Leu Phe Ala Thr
 10 15 20

tgt ttt tta gcg agc ctc atg ttt ttt tgg gaa cca atc gat aat cac 572
 Cys Phe Leu Ala Ser Leu Met Phe Phe Trp Glu Pro Ile Asp Asn His
 25 30 35

ta: ga: ttt gtg aat gat acc ctg tct ctt aag cac acc tca gcg ggg 668
 Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu Lys His Thr Ser Ala Gly
 50 60 65 70

cc^t sq: tac caa tac ttg att aac cac aag gaa aag tgt caa gct caa 716
 Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys Glu Lys Cys Gln Ala Gln
 75 80 85

gac gtc ctc ctt tta ctg ttt gta aaa act	gtc cct gaa aac tat gat	764
Asp Val Leu Leu Leu Phe Val Lys Thr Ala Pro Glu Asn Tyr Asp		
90	95	100
cga cgt tcc gga att aga agg acg tgg ggc aat gaa aat tat gtt cgg		812
Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly Asn Glu Asn Tyr Val Arg		
105	110	115
tct cag ctg aat gcc aac atc aaa act ctg ttt gcc tta gaa act cct		860
Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu Phe Ala Leu Gly Thr Pro		
120	125	130
aat cca ctg gag gga gaa gaa tta ctt aag aaa ctg gct tgg gaa gat		908
Asn Pro Leu Glu Gly Glu Leu Gln Arg Lys Leu Ala Trp Glu Asp		
135	140	145
caa cgg tcc aat gat ata att gag taa gag ttt gtt gat tct ttc taa		956
Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp Phe Val Asp Ser Phe Tyr		
155	160	165
aat tt t a-t ctg a-a tta ctt a-tg cag ttc a-gt tgg gca a-t a-c t-t		1004
Asn Leu Thr Leu Lys Leu Leu Met Gln Phe Ser Trp Ala Asn Thr Tyr		
170	175	180
tgt tca c-t gcc a-a ttt ctt a-tg a-c t	gt	1052
Sys Pro His Ala Lys Phe Leu Met Thr Ala Asp Asp Asp Ile Phe Ile		
185	190	195
cac atg ttt aat ctg att gag tac ttg ctt ctt a-gt tta gaa ctt att ggt		1100
His Met Pro Asn Leu Ile Glu Tyr Leu Gln Ser Leu Glu Gln Ile Gly		
205	210	215
gtt ttt a-t gtc ttt tgg att ggt cgt ttg cat cgt a-gt gtc ctt ccc att		1148
Val Gln Asp Phe Trp Ile Gly Arg Val His Arg Gly Ala Pro Pro Ile		
215	220	225
		230
aga ttt a-t a-c a-c a-a ttt ttt ttt gaa a-tg ttt a-c a-g ttt		1196
Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser Tyr Glu Met Tyr Gln Trp		
235	240	245
cc-t a-t t-t ccc ttt ttt a-t		1244
Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala Ala Tyr Val Ile Ser Gly		
250	255	260
gat ttt a-t gtt gcc a-a gtc ttt ttt a-t gtt gca ttt gtt a-t a-t a-t		1292
Asp Val Ala Ala Lys Val Tyr Gln Ala Ser Gln Thr Leu Asn Ser Ser		
265	270	275
ctt ttt a-t a-t gac ttt gtg ttc a-t gtc ctt ttt gtt a-t a-t a-t a-t		1340
Leu Tyr Ile Asp Asp Val Phe Met Gly Leu Cys Ala Asn Lys Ile Gly		
280	285	290
ata ttt ctt		1388
Ile Val Pro Gln Asp His Val Phe Phe Ser Gly Glu Gly Lys Thr Pro		
295	300	305
		310
tat cat ccc ttt a-t a-t gaa a-a a-t gtt a-t a-t a-t a-t a-t a-t a-t		1436
Tyr His Pro Cys Ile Tyr Glu Lys Met Met Thr Ser His Gly His Leu		
315	320	325

gaa gat ctc cag gac ctt tgg aag aat gct aca gat cct aaa gta aaa 1484
 Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala Thr Asp Pro Lys Val Lys
 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400
 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

acc att tcc aaa ggc ttt ttt ggt caa ata tac tgc aga tta atg aag 1532
 Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile Tyr Cys Arg Leu Met Lys
 345 350 355

ata att ctc ctt tgt aaa att agc tat gtg gac aca tac cct tgt agg 1581
 Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val Asp Thr Tyr Pro Cys Arg
 360 365 370

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Ala Ala Phe Ile
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<210> 2
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<212> PRT
<213> Homo sapiens

<400> 2

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Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr
35 40 45
Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu
50 55 60
Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys
65 70 75 80
Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr
85 90 95
Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly
100 105 110
Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu
115 120 125
Phe Ala Leu Gly Thr Pro Asn Pro Leu Gln Gly Gln Glu Leu Gln Arg
130 135 140
Lys Leu Ala Trp Gln Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp
145 150 155 160
Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe
165 170 175
Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala
180 185 190
Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Gln Tyr Leu Gln
195 200 205
Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His
210 215 220
Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser
225 230 235 240
Tyr Gln Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala
245 250 255
Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Gln Ala Ser
260 265 270
Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu
275 280 285
Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser
290 295 300
Gly Gln Gly Lys Tyr Pro Tyr His Pro Cys Ile Tyr Gln Lys Met Met
310 315 320
Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala
325 330 335
Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile
340 345 350
Tyr Lys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val
355 360 365
Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile
370 375

<210> 3

<211> 1134

<212> DNA

<213> Homo sapiens

<2200>
<221> CDS
<222> (1)...(1134)

<400> 3

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att gag tta ttt gct act ttt tta gct agc ctc atg ttt ttt tgg 96
Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp
20 25 30

aaa cca atc gat aat cac att gtc agc cat atg aag tca tat tct tac 144
Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr
35 40 45

aga tac ctc ata aat agg tat gag ttt gtc aat gat acc ctc tat ctt 192
Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu
50 55 60

agg cac acc tca gcg ggg cct cgc tac caa tac ttt att aac cac aag 240
Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys
65 70 80

aaa aag ttt caa gct caa gag gtc ctc ctt tta ctc ttt gta aaa act 288
Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr
85 90 95

ttt cct gaa aac tat gat cca cgt tcc gga att aga agg agg tgg ggc 336
Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Phe Trp Gly
100 105 110

aat gaa aat tat gtt cgg tct cag ctg aat gcc aac atc aaa act ctg 384
Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu
115 120 125

ttt gcs tta gga act cct aat cca ctg gag gga gaa gaa cta caa aga 432
Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Gln Glu Leu Gln Arg
130 135 140

aaa ctg gct tgg gaa gat caa agg tac aat gat ata att cag caa gac 480
Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp
145 150 155 160

ttt gtt gat tct ttc tac aat ctt act ctg aaa tta ctt atg cag ttc 528
Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe
165 170 175

agt tgg gca aat acc tat ttt cca cat gcc aaa ttt ctt atg act gct 576
Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala
180 185 190

aat gat gac ata ttt att cac atg cca aat ctg att gag tac ctt caa 624
Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Gln Tyr Leu Gln
195 200 205

agt tta gaa caa att ggt gtt caa gag ttt tgg att ggt cgt gtt cat 672
Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His
210 215 220

cg~~t~~ ggt gcc cct ccc att aga gat aaa agc agc aaa tac tac gtg tcc 720
Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser
225 230 235 240

tat gaa atg tac cag tgg cca gct tac cct gac tac aca gcc gga gct 768
Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala
245 250 255

gcc tat gta atc tcc ggt gat gta gct gcc aaa gtc tat gag gca tca 816
Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser
260 265 270

c~~aq~~ aca cta aat tca a~~gt~~ ctt tac ata gac gat gtg ttc atg ggc ctc 864
Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu
275 280 285

tgt gcc aat aaa ata ggc ata gta ccg c~~aq~~ gac cat gtg ttt ttt tct 912
Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser
290 295 300

gga gag ggt aaa act cct tat cat ccc tgc atc tat gaa aac atg atg 960
Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met
305 310 315 320

aca tct cat gga c~~a~~ tta gaa gat ctc c~~aq~~ gac ctt tgg a~~aq~~ aat gct 1008
Thr Ser His Gly His Leu Glu Asp Leu Glu Asp Leu Trp Lys Asn Ala
325 330 335

a~~ca~~ gat cct aaa gta aac a~~cc~~ att tcc aaa ggt ttt ttt gat caa ata 1056
Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile
340 345 350

tac tgc aga tta atg aag ata att ctc ctt tgt aaa att agc tat gtg 1104
Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val
355 360 365

gac aca tac cct tgt agg gct qc~~g~~ ttt atc 1134
Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile
370 375